

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: LONZA AG
- (B) STREET: Muenchensteinerstrasse 38
- (C) CITY: Basle
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE: 4002

(ii) TITLE OF INVENTION: Process for the preparation of (S)- or (R)-3,3,3-trifluoro-2-hydroxy-2-methylpropionic acid

(iii) NUMBER OF SEQUENCES: 14

## (iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (c) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: Klebsiella oxytoca
- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

## (vii) PROVENANCE:

- (B) CLONE(S): pPRS2a

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(197..1181)
- (D) OTHER INFORMATION: /product= "amidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGGA	ACT	CCATGTGGCC	GTGATCCTGG	TCGAGCAGGA	TATTGCGATG	ATCCAGCGGG	60						
CCGCACAGCG	CTGTGCGGTA	ATG	GATAAAG	GCCTGGTTGT	AGAAAACGCTG	ACCCAACAAC	120						
AGCTCTCTGA	TGATCTTTTA	ATGCGTCGTC	ATCTGGCTCT	GTA	ACTAAAC	GCTATAAATT	180						
ACGTGGAGAA	TAACAT	ATG	AAA	TGG	TIG	GAA	GAA	TCC	ATT	ATG	GCC	AAA	229
	Met	Lys	Trp	Leu	Glu	Glu	Ser	Ile	Met	Ala	Lys		
	1				5				10				

CGC	GGT	GTT	GGT	GCC	GGG	CGT	AAA	CCG	GTA	ACG	CAT	CAC	CTG	ACG	GAA	277
Arg	Gly	Val	Gly	Ala	Gly	Arg	Lys	Pro	Val	Thr	His	His	Leu	Thr	Glu	
			15					20					25			
GAA	ATG	CAA	AAA	GAG	TTT	CAT	TAC	ACC	ATT	GGC	CCT	TAT	TCC	ACA	CCC	325
Glu	Met	Gln	Lys	Glu	Phe	His	Tyr	Thr	Ile	Gly	Pro	Tyr	Ser	Thr	Pro	
		30					35					40				
GTC	CTG	ACC	ATC	GAA	CCC	GGT	GAC	CGG	ATT	ATT	GTC	GAC	ACT	CGA	GAT	373
Val	Leu	Thr	Ile	Glu	Pro	Gly	Asp	Arg	Ile	Ile	Val	Asp	Thr	Arg	Asp	
	45					50					55					
GCT	TTT	GAA	GGT	GCT	ATC	AAT	TCG	GAA	CAG	GAT	ATT	CCG	AGC	CAG	TTG	421
Ala	Phe	Glu	Gly	Ala	Ile	Asn	Ser	Glu	Gln	Asp	Ile	Pro	Ser	Gln	Leu	
	60				65					70					75	
CTA	AAA	ATG	CCC	TTT	CTC	AAC	CCA	CAA	AAC	GGA	CCG	ATC	ATG	GTC	AAT	469
Leu	Lys	Met	Pro	Phe	Leu	Asn	Pro	Gln	Asn	Gly	Pro	Ile	Met	Val	Asn	
			80						85					90		
GGC	GCG	GAG	AAA	GGT	GAT	GTG	CTC	GCT	GTC	TAT	ATC	GAA	TCC	ATG	TTG	517
Gly	Ala	Glu	Lys	Gly	Asp	Val	Leu	Ala	Val	Tyr	Ile	Glu	Ser	Met	Leu	
			95					100					105			
CCC	CGC	GGC	GTT	GAT	CCC	TAC	GGC	ATC	TGC	GCC	ATG	ATT	CCG	CAT	TTT	565
Pro	Arg	Gly	Val	Asp	Pro	Tyr	Gly	Ile	Cys	Ala	Met	Ile	Pro	His	Phe	
		110					115					120				
GGC	GGA	CTG	ACC	GGG	ACC	GAC	CTG	ACG	GCC	ATG	CTC	AAT	GAT	CCG	CTG	613
Gly	Gly	Leu	Thr	Gly	Thr	Asp	Leu	Thr	Ala	Met	Leu	Asn	Asp	Pro	Leu	
	125					130					135					
CCA	GAA	AAG	GTG	CGC	ATG	ATT	AAA	CTC	GAC	AGT	GAA	AAG	GTC	TAC	TGG	661
Pro	Glu	Lys	Val	Arg	Met	Ile	Lys	Leu	Asp	Ser	Glu	Lys	Val	Tyr	Trp	
	140				145					150					155	
AGC	AAA	CGC	CAT	ACG	CTT	CCC	TAT	AAA	CCC	CAT	ATT	GGC	ACC	TTG	AGC	709
Ser	Lys	Arg	His	Thr	Leu	Pro	Tyr	Lys	Pro	His	Ile	Gly	Thr	Leu	Ser	
			160						165					170		
GTA	TCG	CCA	GAA	ATT	GAC	TCA	ATC	AAT	TCA	CTG	ACG	CCA	GAC	AAT	CAC	757
Val	Ser	Pro	Glu	Ile	Asp	Ser	Ile	Asn	Ser	Leu	Thr	Pro	Asp	Asn	His	
		175						180					185			
GGC	GGG	AAT	ATG	GAT	GTG	CCG	GAT	ATA	GGA	CCA	GGG	AGT	ATT	ACC	TAT	805
Gly	Gly	Asn	Met	Asp	Val	Pro	Asp	Ile	Gly	Pro	Gly	Ser	Ile	Thr	Tyr	
		190					195					200				
CTG	CCG	GTA	CGT	GCG	CCT	GGA	GGC	CGC	CTG	TTT	ATT	GGT	GAT	GCC	CAT	853
Leu	Pro	Val	Arg	Ala	Pro	Gly	Gly	Arg	Leu	Phe	Ile	Gly	Asp	Ala	His	
	205					210					215					
GCT	TGT	CAG	GGT	GAT	GGT	GAG	ATT	TGC	GGG	ACC	GCA	GTA	GAG	TTT	GCC	901
Ala	Cys	Gln	Gly	Asp	Gly	Glu	Ile	Cys	Gly	Thr	Ala	Val	Glu	Phe	Ala	
	220				225					230					235	
TCA	ATC	ACC	ACC	ATC	AAA	GTC	GAT	TTG	ATC	AAG	AAC	TGG	CAG	CTT	TCC	949
Ser	Ile	Thr	Thr	Ile	Lys	Val	Asp	Leu	Ile	Lys	Asn	Trp	Gln	Leu	Ser	
			240						245					250		
TGG	CCA	CGA	ATG	GAG	AAT	GCC	GAA	AAT	ATT	ATG	AGT	ATT	GGC	AGT	GCA	997
Trp	Pro	Arg	Met	Glu	Asn	Ala	Glu	Asn	Ile	Met	Ser	Ile	Gly	Ser	Ala	
			255					260					265			

CGT CCG CTG GAG GAT GCG ACG CGA ATT GCA TAT CGC GAC TTA ATT TAC	1045
Arg Pro Leu Glu Asp Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr	
270 275 280	
TGG CTG GTA GAA GAC TTT GGC TTC GAA CAA TGG GAT GCC TAC ATG CTT	1093
Trp Leu Val Glu Asp Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu	
285 290 295	
CTG AGT CAA TGC GGC AAA GTG CGG CTG GGC AAC ATG GTC GAC CCC AAA	1141
Leu Ser Gln Cys Gly Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys	
300 305 310 315	
TAC ACC GTT GGC GCG ATG CTG AAC AAA AAC CTG TTA GTT TAGTAGGAAT	1190
Tyr Thr Val Gly Ala Met Leu Asn Lys Asn Leu Leu Val	
320 325	
AACTAACCGG TGAACATTAC CCGGATGTAG ATCGGGGTAA TGTGTAAGTT CAAACAATCG	1250
CTATTTTAA CAGCTAAAGC AGGTGCATAT GGGGCCAGAT ACACCCATCA ATATTGGTTT	1310
ACTTTACTCC TTCAGCGGAG TGACGGCGGC ACAAGAGTTG TCACAATGGC GCGGAGCAAC	1370
CCAGGCTATT GCCGAAATTA ATCAAAATGG CGGCATCAAC GGCAGACCAC TCAATGCAAT	1430
TCATTTGGAT CC	1442

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala	
1 5 10 15	
Gly Arg Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys Glu	
20 25 30	
Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile Glu	
35 40 45	
Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp Ala Phe Glu Gly Ala	
50 55 60	
Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu Leu Lys Met Pro Phe	
65 70 75 80	
Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala Glu Lys Gly	
85 90 95	
Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg Gly Val Asp	
100 105 110	
Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe Gly Gly Leu Thr Gly	
115 120 125	
Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu Pro Glu Lys Val Arg	
130 135 140	

Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp Ser Lys Arg His Thr  
 145 150 155 160  
 Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser Val Ser Pro Glu Ile  
 165 170 175  
 Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His Gly Gly Asn Met Asp  
 180 185 190  
 Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr Leu Pro Val Arg Ala  
 195 200 205  
 Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His Ala Cys Gln Gly Asp  
 210 215 220  
 Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala Ser Ile Thr Thr Ile  
 225 230 235 240  
 Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser Trp Pro Arg Met Glu  
 245 250 255  
 Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg Pro Leu Glu Asp  
 260 265 270  
 Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr Trp Leu Val Glu Asp  
 275 280 285  
 Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu Leu Ser Gln Cys Gly  
 290 295 300  
 Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys Tyr Thr Val Gly Ala  
 305 310 315 320  
 Met Leu Asn Lys Asn Leu Leu Val  
 325

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

## (ii) MOLECULE TYPE: peptide

## (vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala  
 1 5 10 15  
 Ser Arg Lys Pro  
 20

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Tyr Trp Ser Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Thr Val Gly Ala Met Leu Asn Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Trp Leu Glu Glu Ser Ile Met Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala  
1 5 10 15

Glu Lys

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: not known  
(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1  
(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln  
1                      5                      10                      15

Leu Leu Lys

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not known  
(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1  
(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile  
1                      5                      10                      15

Glu Pro Gly Asp Arg  
20

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not known  
(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1  
(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Phe Ile Gly Asp Ala His Ala Glu Gln Gly Asp Gly Glu Ile Glu

1                      5                      10                      15

Gly Thr Ala Val Glu Phe Ala  
20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not known  
(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1  
(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not known  
(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (C) INDIVIDUAL/ISOLATE: PRS1

(vii) **PROVENANCE:**

- (B) CLONE(S) : PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gly Val Asp Pro Tyr Gly Ile Glu Ala Met Ile Pro His Phe Gly Gly  
1 5 10 15

Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Gin Leu Gin Pro  
20 25 30

**Lys**